

Raw Sequence Listing

Patent Application: US/09/430,590D

DATE: 04/17/2001

TIME: 14:36:46

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04172001\I430590D.raw

3 <110> APPLICANT: Poulter, et al.
 5 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS
 7 <130> FILE REFERENCE: 674521-2001.1
 9 <140> CURRENT APPLICATION NUMBER: 09/430,590D
 10 <141> CURRENT FILING DATE: 1999-10-29
 12 <150> PRIOR APPLICATION NUMBER: 60/106,342
 13 <151> PRIOR FILING DATE: 1998-10-30
 15 <160> NUMBER OF SEQ ID NOS: 156
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 388
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Candida albicans
 24 <300> PUBLICATION INFORMATION:
 25 <308> DATABASE ACCESSION NO: AF043301
 26 <309> DATABASE ENTRY DATE: 1998-07-21
 27 <313> RELEVANT RESIDUES: (1)..(388)
 29 <400> SEQUENCE: 1
 30 tgttcgctat agagagattt cctagccgga atgcacgaca atcctgagac ggaagtgcat 60
 32 cgtcgatgcc catggtgcggt ggtaaaaat ttcttagaa aatttgtct ttccctcaac 120
 34 tgcttttaag aaagagaggt tcaagtgggt taagtacgac ggtcacaaag attgcggcgtt 180
 36 atgaggccccg aactgagttt aaataaaaaa tcaagatata attatataacc ttacttgtcc 240
 38 atattgtttt ataatacatt cttagatata tttaatttct gtgtatcaac ctataaaaaca 300
 40 gagatacatt cagtgcattt agtatactga gtgaactggg acctgtgaca ttcaagataa 360
 42 ctgtttcgcg cacgctggca gacgacaa 388
 45 <210> SEQ ID NO: 2
 46 <211> LENGTH: 400
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Candida albicans
 50 <300> PUBLICATION INFORMATION:
 51 <308> DATABASE ACCESSION NO: Y08494
 52 <309> DATABASE ENTRY DATE: 1997-08-27
 53 <313> RELEVANT RESIDUES: (1)..(400)
 55 <400> SEQUENCE: 2
 56 cgggttaatg tatatttcga cttgcaggac ctatagaaca gctgttagatg taaaacactaa 60
 58 tatgaagaac tggaaaaaca ataacttota ttctgactct gattctgtat gaaaactaac 120
 60 tgaagaaaaag aatataaaaaa tataaaaatataaagaagac aaaggagaat ctctgaccct 180
 62 tatatagacc gaaaactaga gtgacgatga accatcagac cagtcaataa ccaactaatt 240
 64 taataatatac aataactcgta ctaacgaggt gtaaacaaaaa taccgaaaaat agaaatataa 300
 66 ataactcaat gccaagatgg tgccaaacca ccaaggtaat aaacaaccaa tagaaccaag 360
 68 aattgttaaat cagacaacga gcaaggctga ttataacaaca 400
 71 <210> SEQ ID NO: 3
 72 <211> LENGTH: 6426
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Candida albicans
 76 <220> FEATURE:
 77 <221> NAME/KEY: CDS

Does Not Comply
Corrected Diskette Needed

See p. 6

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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78 <222> LOCATION: (398)...(1372)
 79 <223> OTHER INFORMATION: ORF1 coding sequence for gag
 82 <220> FEATURE:
 83 <221> NAME/KEY: CDS
 84 <222> LOCATION: (1373)...(6103)
 85 <223> OTHER INFORMATION: ORF2 - coding sequence for pol
 88 <400> SEQUENCE: 3
 89 tgggtttg tgcaattt tggcagaa actgatcaat gaaaatgatg gttattatga 60
 91 gaatggaaaa tttttccatc acacatcagg tggatgacaga actaaactat atttgttagt 120
 93 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
 95 tcaatatata tcttgtgaat aataacttcg ttcttaattca ctatacacaa cttagacgtgt 240
 97 acacgctcaa ttcaggtaa agaaagttaa tattccatca gattagaagt cgatagtgtat 300
 99 aatcatttcg tcccaaatta gcgttgtata aattcagtcc tcagattgtt attattgatt 360
 101 gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat 415
 102 103 Met Ser Ser Ala Lys Asn 1 5
 105 gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct 463
 106 Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala
 107 10 15 20
 109 att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc 511
 110 Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe
 111 25 30 35
 113 ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc 559
 114 Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser
 115 40 45 50
 117 gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc 607
 118 Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro
 119 55 60 65 70
 121 gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag 655
 122 Asp Val Leu Glu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys
 123 75 80 85
 125 gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg 703
 126 Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met
 127 90 95 100
 129 tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tot aag 751
 130 Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys
 131 105 110 115
 133 cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat 799
 134 Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr
 135 120 125 130
 137 gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg 847
 138 Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu
 139 135 140 145 150
 141 ctg aag ttt gta aac gtt gaa cat gag tta gtc gtt tgc tat aac ctt 895
 142 Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu
 143 155 160 165
 145 cca tat ttg ctg cag gtc gaa gag aaa ctt gag gaa ata ctc tac aac 943
 146 Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn
 147 170 175 180

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149	act tca aac gtt gtc gat gag tat gtc cgt agt ctt cca aat ctc ata	991
150	Thr Ser Asn Val Val Asp Glu Tyr Val Arg Ser Leu Pro Asn Leu Ile	
151	185 190 195	
153	ggt caa gtc ttg tac ttc aat cat gtg aag aaa tca gag gct tta agt	1039
154	Gly Gln Val Leu Tyr Phe Asn His Val Lys Lys Ser Glu Ala Leu Ser	
155	200 205 210	
157	ttg ttt ttg aat att cat gcc tca tac tac tca aag tgg att caa gct	1087
158	Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr Ser Lys Trp Ile Gln Ala	
159	215 220 225 230	
161	gac aat gat aca tca gta ctc cca agt tgc tct acc ata gct gaa gaa	1135
162	Asp Asn Asp Thr Ser Val Leu Pro Ser Cys Ser Thr Ile Ala Glu Glu	
163	235 240 245	
165	atg tgt gat cat cct gat tat gct aga ttg gtt gac att cca agc aac	1183
166	Met Cys Asp His Pro Asp Tyr Ala Arg Leu Val Asp Ile Pro Ser Asn	
167	250 255 260	
169	aaa tat gaa ctt aat ctt att gtt agt tta cca gca cca gag aaa cca	1231
170	Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu Pro Ala Pro Glu Lys Pro	
171	265 270 275	
173	aaa gga aaa cca gag gag aac tca ctg gaa caa tct caa aag aag aac	1279
174	Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu Gln Ser Gln Lys Lys Asn	
175	280 285 290	
177	ctg aaa tca aga aag aga aat aag aaa cat cca aaa tca gat aac gat	1327
178	Ser Lys Ser Arg Lys Arg Asn Lys Lys His Pro Lys Ser Asp Asn Asp	
179	295 300 305 310	
181	aaa ggt gaa aaa gaa aaa gaa aaa gaa aaa act tca ctg gaa' tga 'aaa	1375
182	Lys Gly Glu Lys Glu Lys Glu Lys Lys Thr Ser Ser Glu Lys	
183	315 320 325	
185	aca ggt gct gct tct att aat tgt gta atg aat ata cat aat tgc agc	1423
186	Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys Ser	
187	330 335 340	
189	aaa acc acg ttt cca gta gaa aat tct cat tct ctt aat gct tct ttg	1471
190	Lys Thr Thr Phe Pro Val Glu Asn Ser His Ser Leu Asn Ala Ser Leu	
191	345 350 355	
193	aac gta atg aat ttt aaa ggt tta agg ttt aac aag tat cta gtg tat	1519
194	Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val Tyr	
195	360 365 370	
197	gat act ggt gcc aca ata tct gtt gtg aac aat aaa gat ata ttg ctg	1567
198	Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu Ser	
199	375 380 385	
201	aat gtt aag gac gca aca att gaa gtt tct gtt gct gat ggt gct aca	1615
202	Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala Thr	
203	390 395 400 405	
205	tta gaa gca gat tgt att ggt gat cta att atc aga gtc ggt att gtc	1663
206	Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile Val	
207	410 415 420	
209	tcg att acg tta gag aat aca ttg tat tta cca gaa agt tcc ttt aat	1711
210	Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe Asn	
211	425 430 435	
213	ctt gtg agt ttg aaa caa att gaa gaa cga gga ttt aat gtt ctt att	1759

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214	Leu	Val	Ser	Leu	Lys	Gln	Ile	Glu	Glu	Arg	Gly	Phe	Asn	Val	Leu	Ile	
215	440				445			450									1807
217	act	aaa	gaa	tca	gtg	att	gta	ttt	aac	caa	aat	gtg	gct	cct	act	att	
218	Thr	Lys	Glu	Ser	Val	Ile	Val	Phe	Asn	Gln	Asn	Val	Ala	Pro	Thr	Ile	
219	455				460			465									1855
221	att	gct	tca	agg	aag	aat	gct	gct	gat	ctt	tat	atg	ggt	cct	caa	ttc	
222	Ile	Ala	Ser	Arg	Lys	Asn	Ala	Ala	Asp	Leu	Tyr	Met	Gly	Pro	Gln	Phe	
223	470				475			480								485	
225	agt	gaa	gaa	tct	tta	gaa	tgt	gat	ttt	gat	tat	gat	ggt	ttg	gca	gat	1903
226	Ser	Glu	Glu	Ser	Leu	Glu	Cys	Asp	Phe	Asp	Tyr	Asp	Gly	Leu	Ala	Asp	
227					490			495							500		
229	atg	ttg	tcc	aat	gct	aac	caa	gat	gac	aaa	gat	aaa	tca	agt	atg	aat	
230	Met	Leu	Ser	Asn	Ala	Asn	Gln	Asp	Asp	Lys	Asp	Lys	Ser	Ser	Met	Asn	
231					505			510							515		
233	gaa	atg	tca	gaa	tat	caa	gaa	cat	gat	tat	agt	tct	cga	gca	tta	ata	1999
234	Glu	Met	Ser	Glu	Tyr	Gln	Glu	His	Asp	Tyr	Ser	Ser	Arg	Ala	Leu	Ile	
235					520			525							530		
237	aat	tct	ttg	acg	gag	gtt	gat	ttt	gat	gtt	gaa	att	tcc	cca	tat		2047
238	Asn	Ser	Leu	Thr	Glu	Val	Asp	Val	Leu	Asp	Val	Glu	Ile	Ser	Pro	Tyr	
239					535			540							545		
241	gga	gtt	gaa	caa	ttg	cta	cca	act	gga	gat	aag	aac	gat	att	tat	aat	2095
242	Gly	Val	Glu	Gln	Leu	Leu	Pro	Thr	Gly	Asp	Lys	Asn	Asp	Ile	Tyr	Asn	
243					550			555							560		565
245	tcc	cat	ttg	atg	tca	aat	cat	atg	tcc	att	gag	aaa	atc	ttg	ttg	tta	2143
246	Phe	His	Leu	Met	Ser	Asn	His	Met	Ser	Ile	Glu	Lys	Ile	Leu	Leu		
247					570			575							580		
249	caa	aaa	tac	cag	ggt	ctc	gta	ctt	cac	act	tca	aaa	gag	agt	ctt	caa	2191
250	Gln	Lys	Tyr	Gln	Gly	Leu	Val	Leu	His	Thr	Ser	Lys	Glu	Ser	Leu	Gln	
251					585			590							595		
253	aag	att	gct	gtt	aag	gta	tgt	cta	tta	tcg	aat	gcc	aaa	cag	aga		2239
254	Lys	Ile	Ala	Asp	Cys	Lys	Val	Cys	Leu	Leu	Ser	Asn	Ala	Lys	Gln	Arg	
255					600			605							610		
257	agt	cac	aat	cat	cat	tca	gaa	aga	aaa	gcc	tcg	aga	aga	cat	gag	aga	2287
258	Ser	His	Asn	His	His	Ser	Glu	Arg	Lys	Ala	Ser	Arg	Arg	His	Glu	Arg	
259					615			620							625		
261	ctt	cat	tgt	gat	act	ctc	ggt	cca	ttt	agg	tcc	gaa	aat	aac	aag	tgg	2335
262	Leu	His	Cys	Asp	Thr	Leu	Gly	Pro	Phe	Arg	Ser	Glu	Asn	Asn	Lys	Trp	
263					630			635							640		645
265	tat	tta	acg	tct	gtt	ata	gat	gaa	cat	acg	ggt	tac	att	gaa	gga	att	2383
266	Tyr	Leu	Thr	Ser	Val	Ile	Asp	Glu	His	Thr	Gly	Tyr	Ile	Glu	Gly	Ile	
267					650			655							660		
269	att	act	aaa	gac	aga	aag	gta	aag	gat	ctc	tta	att	caa	cga	tta	aag	2431
270	Ile	Thr	Lys	Asp	Arg	Lys	Val	Lys	Asp	Leu	Leu	Ile	Gln	Arg	Leu	Lys	
271					665			670							675		
273	atc	tgg	aat	aat	cgg	ttt	aac	gat	aag	gtg	gca	tac	ttc	aga	agt	gat	2479
274	Ile	Trp	Asn	Asn	Arg	Phe	Asn	Asp	Lys	Val	Ala	Tyr	Phe	Arg	Ser	Asp	
275					680			685							690		
277	aat	gct	cct	gag	ttc	cca	caa	cct	tct	gat	tta	gct	gag	ttc	ggt	att	2527
278	Asn	Ala	Pro	Glu	Phe	Pro	Gln	Pro	Ser	Asp	Leu	Ala	Glu	Phe	Gly	Ile	

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279	695	700	705		2575
281	tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc				
282	Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala				
283	710	715	720	725	2623
285	gag gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg				
286	Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val				
287	730	735	740	740	2671
289	aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat				
290	Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr				
291	745	750	755	755	2719
293	tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa				
294	Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln				
295	760	765	770	770	2767
297	acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg				
298	Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg				
299	775	780	785	785	2815
301	ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa				
302	Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu				
303	790	795	800	805	2863
305	aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc				
306	Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile				
307	810	815	820	820	2911
309	atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg				
310	Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val				
311	825	830	835	835	2959
313	ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt				
314	Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg				
315	840	845	850	850	3007
317	ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc				
318	Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser				
319	855	860	865	865	3055
321	act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga				
322	Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly				
323	870	875	880	885	3103
325	agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt				
326	Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser				
327	890	895	900	900	3151
329	gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat				
330	Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr				
331	905	910	915	915	3199
333	tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac				
334	Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn				
335	920	925	930	930	3247
337	gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc				
338	Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro				
339	935	940	945	945	3295
341	gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg				
342	Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met				
343	950	955	960	965	

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L:1161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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 L:1199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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L:8916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139
L:9648 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:147
L:9660 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:148
L:9672 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:149
L:9684 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:150
L:9696 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:151
L:9708 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:152
L:9720 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:153
L:9732 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:154
L:9744 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:155
L:9756 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:156